

SEQUENCE LISTING

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 Nilsson, Dan
 SOERENSEN, Kim I.

<120> METHOD OF IMPROVING THE EFFICACY OF LACTIC ACID BACTERIAL STARTER
 CULTURES AND IMPROVED STARTER CULTURE COMPOSITIONS

<130> KRINGELUM=1A

<140> 09/879,036

<141> 2001-06-13

<150> US 09/086,722

<151> 1998-05-29

<150> PCT/DK98/00210

<151> 1998-05-25

<150> US 60/048,337

<151> 1997-05-30

<150> DK 0633/97

<151> 1997-05-30

<160> 2

<170> PatentIn version 3.1

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<212> DNA

<213> Lactococcus lactis

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<221> CDS

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 tgacagattt ttttatctaa taattaaaat aattatttca caatgttcac aagcgcttac 180
 aaaagaaaat agattgactt atgctaaact gaataatgta aaaagaattt tacatttaaa 240
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 Met Lys Ile Val Val Ile Gly Thr Asn His Ala Gly
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 att gct aca gcg aat aca tta ctt gaa caa tat ccc ggg cat gaa att 338
 Ile Ala Thr Ala Asn Thr Leu Leu Glu Gln Tyr Pro Gly His Glu Ile
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gtc atg att gac cgt aat agc aac atg agt tat cta ggt tgt ggc aca Val Met Ile Asp Arg Asn Ser Asn Met Ser Tyr Leu Gly Cys Gly Thr 30 35 40	386
gca att tgg gtt gga aga caa att gaa aaa cca gat gaa tta ttt tat Ala Ile Trp Val Gly Arg Gln Ile Glu Lys Pro Asp Glu Leu Phe Tyr 45 50 55 60	434
gcc aaa gca gag gat ttt gag gca aaa ggg gta aaa att ttg act gaa Ala Lys Ala Glu Asp Phe Glu Ala Lys Gly Val Lys Ile Leu Thr Glu 65 70 75	482
aca gaa gtt tca gaa att gat ttt gct aat aag aaa gtt tat gca aaa Thr Glu Val Ser Glu Ile Asp Phe Ala Asn Lys Lys Val Tyr Ala Lys 80 85 90	530
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gca aca ggt tca cgt cca att att cct aat cta cca ggc aaa gac ctt Ala Thr Gly Ser Arg Pro Ile Ile Pro Asn Leu Pro Gly Lys Asp Leu 110 115 120	626
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gga tat atc ggt aca gag att gcg gaa gca gct aaa cgt cgg ggt aaa Gly Tyr Ile Gly Thr Glu Ile Ala Glu Ala Ala Lys Arg Arg Gly Lys 160 165 170	770
gaa gtt ctt ctc ttt gac gct gaa aat act tca ctt gca tca tat tat Glu Val Leu Leu Phe Asp Ala Glu Asn Thr Ser Leu Ala Ser Tyr Tyr 175 180 185	818
gat gaa gaa ttt gcc aaa gga atg gat gaa aac ctt gct caa cat gga Asp Glu Glu Phe Ala Lys Gly Met Asp Glu Asn Leu Ala Gln His Gly 190 195 200	866
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gaa ggt tat gta tca caa atc gta acc aac aag gcg act tat gat gtt Glu Gly Tyr Val Ser Gln Ile Val Thr Asn Lys Ala Thr Tyr Asp Val 225 230 235	962
gat ctt gtc atc aat tgt att ggt ttt act gcc aac agt gcc ttg gca Asp Leu Val Ile Asn Cys Ile Gly Phe Thr Ala Asn Ser Ala Leu Ala 240 245 250	1010
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tca aac gct gtt cgg tca gga att gtc gca gga cac aat att ggt gga Ser Asn Ala Val Arg Ser Gly Ile Val Ala Gly His Asn Ile Gly Gly 305 310 315			1202
aaa gaa tta gaa tct gtt ggt gtt caa ggt tct aat ggt att tcg att Lys Glu Leu Glu Ser Val Gly Val Gln Gly Ser Asn Gly Ile Ser Ile 320 325 330			1250
ttt ggt tac aat atg act tct aca gga ctt tct gtt aaa gct gct aaa Phe Gly Tyr Asn Met Thr Ser Thr Gly Leu Ser Val Lys Ala Ala Lys 335 340 345			1298
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gct tgg ttt ctt cat gaa aac aac gat agt gtg aaa att cgt atc gta Ala Trp Phe Leu His Glu Asn Asn Asp Ser Val Lys Ile Arg Ile Val 365 370 375 380			1394
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<212> PRT

<213> Lactococcus lactis

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Arg Asn Ser Asn Met Ser Tyr Leu Gly Cys Gly Thr Ala Ile Trp Val
35 40 45

Gly Arg Gln Ile Glu Lys Pro Asp Glu Leu Phe Tyr Ala Lys Ala Glu
50 55 60

Asp Phe Glu Ala Lys Gly Val Lys Ile Leu Thr Glu Thr Glu Val Ser
65 70 75 80

Glu Ile Asp Phe Ala Asn Lys Lys Val Tyr Ala Lys Thr Lys Ser Asp
85 90 95

Asp Glu Ile Ile Glu Ala Tyr Asp Lys Leu Val Leu Ala Thr Gly Ser
100 105 110

Arg Pro Ile Ile Pro Asn Leu Pro Gly Lys Asp Leu Lys Gly Ile His
115 120 125

Phe Leu Lys Leu Phe Gln Glu Gly Gln Ala Ile Asp Ala Glu Phe Ala
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Lys Glu Lys Val Lys Arg Ile Ala Val Ile Gly Ala Gly Tyr Ile Gly
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Thr Glu Ile Ala Glu Ala Ala Lys Arg Arg Gly Lys Glu Val Leu Leu
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Phe Asp Ala Glu Asn Thr Ser Leu Ala Ser Tyr Tyr Asp Glu Glu Phe
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Ala Lys Gly Met Asp Glu Asn Leu Ala Gln His Gly Ile Glu Leu His
195 200 205

Phe Gly Gln Leu Ala Lys Glu Phe Lys Ala Asn Glu Glu Gly Tyr Val
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Ser Gln Ile Val Thr Asn Lys Ala Thr Tyr Asp Val Asp Leu Val Ile
225 230 235 240

Asn Cys Ile Gly Phe Thr Ala Asn Ser Ala Leu Ala Ser Asp Lys Leu
245 250 255

Ala Thr Phe Lys Asn Gly Ala Ile Lys Val Asp Lys His Gln Gln Ser
260 265 270

Ser Asp Pro Asp Val Tyr Ala Val Gly Asp Val Ala Thr Ile Tyr Ser
275 280 285

Asn Ala Leu Gln Asp Phe Thr Tyr Ile Ala Leu Ala Ser Asn Ala Val
290 295 300

Arg Ser Gly Ile Val Ala Gly His Asn Ile Gly Gly Lys Glu Leu Glu
305 310 315 320

Ser Val Gly Val Gln Gly Ser Asn Gly Ile Ser Ile Phe Gly Tyr Asn
325 330 335

Met Thr Ser Thr Gly Leu Ser Val Lys Ala Ala Lys Lys Leu Gly Leu
340 345 350

Glu Val Ser Phe Ser Asp Phe Glu Asp Lys Gln Lys Ala Trp Phe Leu
355 360 365

His Glu Asn Asn Asp Ser Val Lys Ile Arg Ile Val Tyr Glu Thr Lys
370 375 380

Ser Arg Arg Ile Ile Gly Ala Gln Leu Ala Ser Lys Ser Glu Ile Ile
385 390 395 400

Ala Gly Asn Ile Asn Met Phe Ser Leu Ala Ile Gln Glu Lys Lys Thr
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Ile Asp Glu Leu Ala Leu Leu Asp Leu Phe Phe Leu Pro His Phe Asn
420 425 430

Ser Pro Tyr Asn Tyr Met Thr Val Ala Ala
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